

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101521,288  
Source: PCT  
Date Processed by STIC: 1-26-05

***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/26/2005

PATENT APPLICATION: US/10/521,288

TIME: 12:55:09

Input Set : A:\11899.0235.PCUS00.ST25.txt

Output Set: N:\CRF4\01262005\J521288.raw

3 <110> APPLICANT: Flasiński, Stanisław  
 5 <120> TITLE OF INVENTION: Methods for Using Artificial Polynucleotides and  
 Compositions  
 6 thereof to Reduce Transgene Silencing  
 8 <130> FILE REFERENCE: 11899.0235.PCUS00  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,288  
 C--> 11 <141> CURRENT FILING DATE: 2005-01-14  
 13 <150> PRIOR APPLICATION NUMBER: US 06/396,665  
 14 <151> PRIOR FILING DATE: 2002-07-18  
 16 <160> NUMBER OF SEQ ID NOS: 35  
 18 <170> SOFTWARE: PatentIn version 3.3  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 515  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Oryza sativa  
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 35 Leu Arg Leu Pro Ala Ala Ala Arg Gly Gly Met Arg Val Arg Val Arg  
 36 35 40 45  
 39 Ala Arg Gly Arg Arg Glu Ala Val Val Val Ala Ser Ala Ser Ser Ser  
 40 50 55 60  
 43 Ser Val Ala Ala Pro Ala Ala Lys Ala Glu Glu Ile Val Leu Gln Pro  
 44 65 70 75 80  
 47 Ile Arg Glu Ile Ser Gly Ala Val Gln Leu Pro Gly Ser Lys Ser Leu  
 48 85 90 95  
 51 Ser Asn Arg Ile Leu Leu Leu Ser Ala Leu Ser Glu Gly Thr Thr Val  
 52 100 105 110  
 55 Val Asp Asn Leu Leu Asn Ser Glu Asp Val His Tyr Met Leu Glu Ala  
 56 115 120 125  
 59 Leu Lys Ala Leu Gly Leu Ser Val Glu Ala Asp Lys Val Ala Lys Arg  
 60 130 135 140  
 63 Ala Val Val Val Gly Cys Gly Gly Lys Phe Pro Val Glu Lys Asp Ala  
 64 145 150 155 160  
 67 Lys Glu Glu Val Gln Leu Phe Leu Gly Asn Ala Gly Ile Ala Met Arg  
 68 165 170 175  
 71 Ser Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val  
 72 180 185 190  
 75 Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile Gly Asp Leu Val  
 76 195 200 205  
 79 Val Gly Leu Lys Gln Leu Gly Ala Asp Val Asp Cys Phe Leu Gly Thr  
 80 210 215 220

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88                245                250                255
91 Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu Ile Ile
92                260                265                270
95 Asp Lys Leu Ile Ser Ile Pro Tyr Val Glu Met Thr Leu Arg Leu Met
96                275                280                285
99 Glu Arg Phe Gly Val Lys Ala Glu His Ser Asp Ser Trp Asp Arg Phe
100                290                295                300
103 Tyr Ile Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala Tyr Val
104 305                310                315                320
107 Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile
108                325                330                335
111 Thr Gly Gly Thr Val Thr Val Gln Gly Cys Gly Thr Thr Ser Leu Gln
112                340                345                350
115 Gly Asp Val Lys Phe Ala Glu Val Leu Glu Met Met Gly Ala Lys Val
116                355                360                365
119 Thr Trp Thr Asp Thr Ser Val Thr Val Thr Gly Pro Pro Arg Glu Pro
120                370                375                380
123 Tyr Gly Lys Lys His Leu Lys Ala Val Asp Val Asn Met Asn Lys Met
124 385                390                395                400
127 Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala Asp Gly
128                405                410                415
131 Pro Thr Ala Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu Thr Glu
132                420                425                430
135 Arg Met Val Ala Ile Arg Thr Glu Leu Thr Lys Leu Gly Ala Ser Val
136                435                440                445
139 Glu Glu Gly Pro Asp Tyr Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn
140                450                455                460
143 Ile Thr Ala Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met Ala Phe
144 465                470                475                480
147 Ser Leu Ala Ala Cys Ala Asp Val Pro Val Thr Ile Arg Asp Pro Gly
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169 ggggggatgc ggggtgcgggt gcgggcgcgc gggcggcgcgc aggcggtggt ggtggcgctcc      180
171 gcgtcgtcgt cgtcgggtggc agcgcgcgcgc gcgaaggcgc aggagatcgt gctccagccc      240
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175 ctctctctct ccgccctctc cgagggcaca acagtgggtgg acaacttgct gaacagtgag      360

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183 gccgtgactg ctgctggtgg aaatgcaact tatgtgcttg atggagtgcc acgaatgagg 600
185 gagagaccga ttggtgactt ggttgctggg ttgaaacaac ttggtgcgga tgtcgactgt 660
187 ttcttggca ctgaatgccc acctgttcgt gtcaagggaa ttggaggact tctggtggc 720
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242 gcggtcacag ccgctggagg caacgcaaca tacgtcctag atggggtgcc gagaatgcgt 600
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278 <211> LENGTH: 1548
279 <212> TYPE: DNA
280 <213> ORGANISM: Oryza sativa
282 <400> SEQUENCE: 4
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287 ggcggcatga gagttagagt gagggtcaga ggtaggcggg aggctgtagt cgtagcctcc 180
289 gcttctagca gttcgggtggc tgcgcgggct gctaaggcag aggagattgt ttacaacct 240
291 attagggaaa tatcggggggc cgtacaatta cctggaagca agagcctttc caacaggatt 300
293 ctggtgcttt cagctctctc ggagggaaca acagttgtgg ataactctgtt gaatagttag 360
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323 cctgacgttg ctatgacact tgccgttggt gccctttttg cagacggccc aacggcgata 1260
325 cgcgatgttg catcatggcg cgtcaaggaa acggagagga tgggtggctat tcgaactgaa 1320
327 ctcaccaaac ttggtgcctc tgtagaggag ggccctgatt actgtatcat tacacccct 1380
329 gagaaactta acatcactgc tattgatata tacgacgac atagaatggc tatggctttc 1440
331 tcactggccg cttgtgcaga tgttcctgtc acaatcagag atcctggctg tactagaaag 1500
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352 35 40 45
355 His Lys Asn Gly Ser Phe Met Gly Asn Phe Asn Val Gly Lys Gly Asn
356 50 55 60
359 Ser Gly Val Phe Lys Val Ser Ala Ser Val Ala Ala Glu Lys Pro
360 65 70 75 80
363 Ser Thr Ser Pro Glu Ile Val Leu Glu Pro Ile Lys Asp Phe Ser Gly

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371	Leu	Ala	Ala	Leu	Ser	Glu	Gly	Thr	Thr	Val	Val	Asp	Asn	Leu	Leu	Tyr
372				115					120					125		
375	Ser	Glu	Asp	Ile	His	Tyr	Met	Leu	Gly	Ala	Leu	Arg	Thr	Leu	Gly	Leu
376				130					135					140		
379	Arg	Val	Glu	Asp	Asp	Lys	Thr	Thr	Lys	Gln	Ala	Ile	Val	Glu	Gly	Cys
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383	Gly	Gly	Leu	Phe	Pro	Thr	Ser	Lys	Glu	Ser	Lys	Asp	Glu	Ile	Asn	Leu
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387	Phe	Leu	Gly	Asn	Ala	Gly	Ile	Ala	Met	Lys	Ser	Leu	Thr	Ala	Ala	Val
388				180						185					190	
391	Val	Ala	Ala	Gly	Gly	Asn	Ala	Ser	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg
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395	Met	Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Ala	Gly	Leu	Lys	Gln	Leu
396				210					215					220		
399	Gly	Ala	Asp	Val	Asp	Cys	Phe	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg
400	225						230					235				240
403	Val	Asn	Gly	Lys	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly
404				245						250					255	
407	Ser	Val	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu
408				260						265					270	
411	Ala	Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Val	Asp	Lys	Leu	Ile	Ser	Val
412				275						280				285		
415	Pro	Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser
416				290					295			300				
419	Val	Glu	His	Ser	Gly	Asn	Trp	Asp	Arg	Phe	Leu	Val	His	Gly	Gly	Gln
420	305					310					315					320
423	Lys	Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Phe	Val	Glu	Gly	Asp	Ala	Ser	Ser
424				325						330					335	
427	Ala	Ser	Tyr	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Gly	Thr	Ile	Thr	
428				340					345					350		
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436				370			375					380				
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440	385					390					395					400
443	Arg	Gly	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr
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447	Leu	Ala	Val	Val	Ala	Leu	Phe	Ala	Asn	Gly	Pro	Thr	Ala	Ile	Arg	Asp
448				420						425				430		
451	Val	Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys
452				435					440					445		
455	Thr	Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Glu	Glu	Gly	Pro	Asp	Tyr
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date